

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 02:08:12 ; Search time 5587 Seconds

(without alignments)

11344.088 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 1308

Sequence: 1 atgcaaggacaggcaggag.....aaaatcccaactaaatccatg 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_dat:*

7: gb_Ph:*

8: gb_Dl:*

9: gb_Dr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1208	100.0	1743	6	AX191430		AX191430 Sequence
2	1208	100.0	1743	6	AX454638		AX454638 Sequence
3	1208	100.0	1743	6	AK91116		AK91116 Sequence
4	1208	100.0	1743	6	AX697167		AX697167 Sequence
5	1208	100.0	1743	9	AY356700		AY356700 Homo sapi
6	1208	100.0	1766	6	AX675079		AX675079 Sequence
7	1208	99.3	1313	6	AR541803		AR541803 Sequence
8	1208	99.3	1710	6	AR560132		AR560132 Sequence
9	1295.2	99.0	1787	9	AY220118		AY220118 Homo sapi
10	1270.4	97.1	1581	6	AX32981		AX32981 Sequence
11	1270.4	97.1	1759	6	AX358862		AX358862 Sequence
12	1263.4	96.6	1329	6	AX135904		AX135904 Sequence
13	1262.4	96.5	1580	6	AX393967		AX393967 Sequence
14	1244.4	95.1	1254	6	CQ756115		CQ756115 Sequence
15	1192.8	90.4	1194	6	AK135908		AK135908 Sequence
16	1097	83.9	1346	9	AY185496		AY185496 Homo sapi
17	1073.4	82.1	1549	9	AY220120		AY220120 Homo sapi
18	872	66.7	1156	9	AY185497		AY185497 Homo sapi
19	859.8	66.5	1489	9	AY220121		AY220121 Homo sapi

ALIGNMENTS

AY220119	Homo sapi	AY220119	9
AL12708	Human chr	CNS01DTA	9
AL12990	Human chr	CNS01DTA	9
BC020747	Homo sapi	BC020747	9
AX409610	Sequence	AX409610	6
M14051	Human thyro	HUMTBG	9
AF204928	Bos tauru	AF204928	4
AR531797	Sequence	AR531797	6
X69795	O.aries mRN	OATBG	4
CQ716276	Sequence	CQ716276	6
AF204929	Sub acro f	AF204929	4
AX01745	Sequence	AX01745	6
AM63991	Rat thyroxi	AY75783	6
AX642662	Sequence	AX642662	6
J05176	Human alpha	BD176851	6
BD176851	A method	BD176851	6
AX770543	Sequence	AX770543	6
AF059747	Homo sapi	AF059747	6
CO802318	Sequence	CO802318	6
CQ814554	Sequence	CQ814554	6
AX612661	Sequence	AX612661	6
41	373.2	28.5	1428
42	373.2	28.5	1528
43	373.2	28.5	1592
44	373.2	28.5	1603
45	373.2	28.5	2480
45	373.2	28.5	28.5
35	373.2	28.5	1428
36	373.2	28.5	1466
37	373.2	28.5	1466
38	373.2	28.5	1522
39	373.2	28.5	1522
40	373.2	28.5	1522
41	373.2	28.5	1522
42	373.2	28.5	1528
43	373.2	28.5	1592
44	373.2	28.5	1603
45	373.2	28.5	2480
45	373.2	28.5	28.5

ORIGIN

RESULT 1			
AX191430			
LOCUS	AX191430	1743 bp	DNA
DEFINITION	Sequence 5 from Patent WO0149715.		
ACCESSION	AX191430		
VERSION	AX191430.1		
KEYWORDS	GI:15209638		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buterria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Ashkenazi, A.J., Goddard, A., Gurney, A.L., Napier, M.A., Watanabe, C.K. and Wood, W.I.		
TITLE	Methods and compositions for inhibiting neoplastic cell growth		
JOURNAL	Patent: WO 019715-A 5 12-JUL-2001; Genentech, Inc (US)		
FEATURES	Location/Qualifiers		
Source	1. 1743 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		

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! nucleic - nucleic search, using bw model!

On: October 9, 2005, 02:01:07 : Search time 723 Seconds
 (without alignments)
 10709.574 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Score: 1308

Sequence: 1 atgaaaggccaggccaggag.....aaaaatcccaactaaatccctag 1308

Origin table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 100%
Listing first 45 summaries

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N_Geneseq16Dec04:*
1: Geneseqm1980s:*
2: Geneseqm1990s:*
3: Geneseqm2000s:*
4: Geneseqm2001as:*
5: Geneseqm2001bs:*
6: Geneseqm2002as:*
7: Geneseqm2002bs:*
8: Geneseqm2003as:*
9: Geneseqm2003bs:*
10: geneseqm2003cs:*
11: Geneseqm2003ds:*
12: Geneseqm2004ab:*
13: Geneseqm2004bs:*
13:

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMATES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1308	100.0	1743	3	ABP37089	Aaa37089 Human P
2	1308	100.0	1743	4	AAE54367	AaaE54367 Primer
3	1308	100.0	1743	4	ABE46150	AabE6150 Human D
4	1308	100.0	1743	6	ABH88183	Abh88183 Human P
5	1308	100.0	1743	6	ABL11752	Abk11752 cDNA en
6	1308	100.0	1743	6	ABN95672	Abn95672 Human a
7	1308	100.0	1743	8	ACB89600	Acb89600 cDNA en
8	1308	100.0	1743	8	ACB99600	Acb99600 Human s
9	1308	100.0	1743	8	ACG05925	Acg05925 Human s
10	1308	100.0	1743	8	ACG66759	Acg66759 cDNA en
11	1308	100.0	1743	8	ACG20334	Acg20334 Human s
12	1308	100.0	1743	8	ACF19720	Acf19720 Human s
13	1308	100.0	1743	8	ACD20008	Acd20008 Human s
14	1308	100.0	1743	8	ACI13173	Aci13173 Human s
15	1308	100.0	1743	8	ACI25276	Aci25276 Human s
16	1308	100.0	1743	8	ACI00325	Aci00325 Human s
17	1308	100.0	1743	8	ACI72382	Aci72382 Novel 1 h
18	1308	100.0	1743	8	ACD04906	Acd04906 Novel 1 h
19	1308	100.0	1743	8	ACD18367	Acd18367 Human s
20	1308	100.0	1743	8	ACD08374	Acd08374 Human s

ALIGNMENTS

RESULT 1	AAA37089	standard	CDNA	1743	BP.
ID	AAA37089				
XX					
AC	AAA37089;				
XX					
DT	08-AUG-2000	(first entry)			
DE	Human PRO1337	(UN0692)	CDNA	sequence	SEQ ID NO:235.
XX					

Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening; 88.

Homo sapiens	WO2000012708-A2.	09-MAR-2000.	01-SEP-1999;	99W0-0020111
			01-SEP-1998;	98US-0098716P
			01-SEP-1998;	98US-0098749P
			01-SEP-1998;	98US-0098780P
			02-SEP-1998;	98US-0098803P
			02-SEP-1998;	98US-0098821P
			02-SEP-1998;	98US-0098843P
			03-SEP-1998;	98US-0099536P
			09-SEP-1998;	98US-0099594P
			09-SEP-1998;	98US-0099602P
			09-SEP-1998;	98US-0099642P
			09-SEP-1998;	98US-0099741P
			10-SEP-1998;	98US-0099754P
			10-SEP-1998;	98US-0099763P
			10-SEP-1998;	98US-0099792P
			10-SEP-1998;	98US-0099808P
			10-SEP-1998;	98US-0099812P
			10-SEP-1998;	98US-0099815P
			10-SEP-1998;	98US-0099816P
			15-SEP-1998;	98US-010388P
			15-SEP-1998;	98US-010389P
			15-SEP-1998;	98US-0100398P

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 03:00:48 ; Search time 4041 Seconds

(without alignments)
12320.79 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Pref. Score: 1308

Sequence: 1 atgcaaggacaggcaggag.....aaatatccactaaatcctag 1308

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: 9b_est1:*

2: 9b_est2:*

3: 9b_hrc:*

4: 9b_est3:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

8: 9b_gbs1:*

9: 9b_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	124.4	95.1	1254	AY401148 Homo sapi
2	114.0	87.2	1228	AY401149 Pan trogl
3	742.6	56.8	906	BG758811 Gorilla, M.
4	735	56.2	813	BG756763 602710234
5	70.4	55.8	1073	BM455692 AGRCOURT
6	725	55.4	1257	AY401150 Mus muscu
7	725	55.4	1694	AK009343
8	708.2	54.1	816	BG684028
9	695.6	53.2	946	BF794222
10	684	52.3	1097	BF975146
11	617.6	47.2	784	BG035642
12	612.2	46.8	702	B187108
13	612.2	46.8	771	BG398393
14	533.4	40.8	576	BF128752
15	377.4	33.6	447	AW408367
16	373.2	28.5	1487	CR609815
17	373.2	28.5	1499	CR619614
18	373.2	28.5	1501	CR590750
19	373.2	28.5	1503	CR612671
20	373.2	28.5	1503	CR623440
21	373.2	28.5	1504	CR620654
22	373.2	28.5	1505	CR595639
23	373.2	28.5	1506	CR592388
24	373.2	28.5	1512	CR605766

RESULTS
1
LOCUS AY401148
DEFINITION Homo sapiens HCM0794 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
AY401148

ACCESSION AY401148.1
VERSION GI:39757137

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 1254)
AUTHORS Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanerbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE This sequence was made by sequencing genomic exons and ordering them based on alignment.

JOURNAL Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES 1. .1254
Source /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1254
/locus_tag="HCM0794"

ORIGIN

Query Match 95.1%; Score 1244.4;
Best Local Similarity 99.5%; Pred. No. 0;

Matches 1248; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 55 ATGGCATCTTACCTTATGGAGTACTCTTGCTGTGGCTCTGCTGATCTACTGT 114
Db 1 ATGGCATCTTACCTTATGGAGTACTCTTGCTGTGGCTCTGCTGATCTACTGT 60

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 03:12:08 ; Search time 258 Seconds
 (without alignments)

2925.542 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 1308

Sequence: 1 atgaaaggcaggcaggag.....aaaaatccactaaatccctag 1308

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gspect 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents NA: *

1: /cgn2_6/podata/1/ina/5A_COMB_seq: *
 2: /cgn2_6/podata/1/ina/5B_COMB_seq: *
 3: /cgn2_6/podata/1/ina/6A_COMB_seq: *
 4: /cgn2_6/podata/1/ina/6B_COMB_seq: *
 5: /cgn2_6/podata/1/ina/pCTUS_COMB_seq: *
 6: /cgn2_6/podata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1298.4	99.3	1313	4 US-09-774-528-51	Sequence 51, Appli
2	1298.4	99.3	1710	4 US-09-528-2	Sequence 2, Appli
3	539.4	41.2	1878	4 US-09-949-016-5670	Sequence 5670, Appli
4	534.6	40.9	1432	4 US-09-119-019-389	Sequence 389, Appli
5	371.2	28.5	5193	4 US-09-376-394-1126	Sequence 1126, Appli
6	371.6	28.4	1580	4 US-09-976-594-18	Sequence 18, Appli
7	371.6	28.4	1580	4 US-09-919-039-18	Sequence 18, Appli
8	326.6	25.0	1527	4 US-09-244-111-7	Sequence 7, Appli
9	306	23.4	1245	4 US-09-949-016-2272	Sequence 2272, Appli
10	306	23.4	1185	3 US-09-023-039-2	Sequence 2, Appli
11	306	23.4	5932	3 US-09-299-141-4	Sequence 4, Appli
12	306	23.4	6142	3 US-09-299-141-8	Sequence 8, Appli
13	306	23.4	6565	3 US-09-299-141-1	Sequence 1, Appli
14	306	23.4	6714	3 US-09-299-141-6	Sequence 6, Appli
15	306	23.4	6924	3 US-09-299-141-9	Sequence 9, Appli
16	306	23.4	6924	3 US-09-299-141-10	Sequence 10, Appli
17	306	23.4	6924	3 US-09-299-141-11	Sequence 11, Appli
18	306	23.4	6981	3 US-09-299-141-11	Sequence 7, Appli
19	306	23.4	7054	3 US-09-299-141-3	Sequence 3, Appli
20	304	23.3	7405	3 US-09-299-141-2	Sequence 2, Appli
21	304	23.3	1417	4 US-10-000-489-91	Sequence 91, Appli
22	289	22.1	8190	4 US-09-949-016-1412	Sequence 1712, Appli
23	288	22.0	1356	1 US-08-002-202-12	Sequence 12, Appli
24	288	22.0	1356	1 US-08-002-202-12	Sequence 18, Appli
25	288	22.0	1356	3 US-08-481-534-12	Sequence 12, Appli
26	288	22.0	1356	3 US-08-481-534-18	Sequence 18, Appli
27	286.4	21.9	1356	1 US-08-002-202-16	Sequence 16, Appli

ALIGNMENTS

28	286.4	21.9	1356	3 US-08-481-534-16	Sequence 16, Appli
29	285.8	21.9	1423	1 US-07-889-954-1	Sequence 1, Appli
30	285.8	21.9	1423	1 US-07-984-423-1	Sequence 1, Appli
31	285.8	21.9	1423	1 US-08-421-891-1	Sequence 1, Appli
32	284.2	21.7	1476	4 US-09-949-016-1726	Sequence 1726, Appli
33	271.2	20.7	1266	4 US-09-949-016-2294	Sequence 2294, Appli
34	260	19.9	1194	4 US-10-000-489-49	Sequence 49, Appli
35	254.4	19.4	1263	4 US-09-949-016-834	Sequence 834, Appli
36	253.8	19.4	1185	3 US-09-023-339-3	Sequence 3, Appli
37	253.8	19.4	1260	3 US-09-023-173-5	Sequence 5, Appli
38	253.8	19.4	1308	3 US-09-023-173-10	Sequence 10, Appli
39	253.8	19.4	1308	3 US-09-023-339-6	Sequence 6, Appli
40	233.4	17.8	1245	4 US-09-055-665-13	Sequence 13, Appli
41	233.4	17.8	1445	4 US-09-061-325-13	Sequence 13, Appli
42	233.4	17.8	1445	4 US-10-012-512-13	Sequence 13, Appli
43	233.4	17.8	1445	4 US-10-015-123-13	Sequence 13, Appli
44	197.6	15.1	1339	1 US-07-959-490-1	Sequence 1, Appli
45	189.2	14.5	8896	4 US-09-949-016-14014	Sequence 14014, Appli

RESULTS

RESULT 1

US-09-774-528-51

Sequence 51, Application US/09774528
 Patent No. 6743619

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 Zhou, Ping
 Goodrich, Ryke
 Liu, Chenghua
 Asundi, Vinod
 Ren, Feiyun
 Zhang, Jie
 Zhao, Qing A.
 Yang, Yonghong
 Xue, Aidong J.
 Wehrman, Tom
 Wang, Jian-Rui.
 APPLICANT: Demnac, Radoje T.
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Jian-Rui.

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 802

CURRENT APPLICATION NUMBER: US/09/774, 528

CURRENT FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO. 51 LENGTH: 1313

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (6)...(1313)

US-09-774-528-51

Query Match 99.3%; Score: 1298.4; DB 4; Length 1313;
 Best Local Similarity 99.5%; Pred. No. 0; Mismatches 6; Gaps 0;

QY 1 ATGCAAGACAGGGCAGGAGAGAGAGACATATTGTCCAAATGGCA 60

Db 6 ATGCAAGACAGGGCAGGAGAGAGACATATTGTCCAAATGGCA 65

QY 61 TCTTAACPTTATGGATCTGGCTCTGGCTCAATCTACTGTGTGTC 120

Db 66 TCTTAACPTTATGGATCTGGCTCTGGCTCAATCTACTGTGTGTC 125

QY 121 CCGGCCATGCCCCATGGCAATCCCCGCCCTTCCTCCACAAAGAGACCCCTGGCTCA 180

Db 126 CCGGCCATGCCCCATGGCAATCCCCGCCCTTCCTCCACAAAGAGACCCCTGGCTCA 185

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2005, 04:52:59 ; Search time 912 Seconds

(without alignments)
9999.049 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 1308

Sequence: 1 atgcaaggacaggcaggag.....aaaatccactaaatcctag 1308

Scoring table: IDENTITY_NUC
Gapext 1.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters:

16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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1: /cgns_6/ptodata/2/pubpna/us07_PUBCOMB.seq:*
 2: /cgns_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 3: /cgns_6/ptodata/2/pubpna/us06_NEW_PUB.seq:*
 4: /cgns_6/ptodata/2/pubpna/us05_NEW_PUB.seq:*
 5: /cgns_6/ptodata/2/pubpna/us07_NEW_PUB.seq:*
 6: /cgns_6/ptodata/2/pubpna/PCTNS_PUBCOMB.seq:*
 7: /cgns_6/ptodata/2/pubpna/us08_NEW_PUB.seq:*
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 9: /cgns_6/ptodata/2/pubpna/us09_PUBCOMB.seq:*
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13: /cm2_6/ptodata/2/pubpna/us10_PUBCOMB.seq:*
14: /cm2_6/ptodata/2/pubpna/us10C_PUBCOMB.seq:*
15: /cm2_6/ptodata/2/pubpna/us10I_PUBCOMB.seq:*
16: /cm2_6/ptodata/2/pubpna/us10N_PUBCOMB.seq:*
17: /cm2_6/ptodata/2/pubpna/us10B_PUBCOMB.seq:*
18: /cm2_6/ptodata/2/pubpna/us10F_PUBCOMB.seq:*
19: /cm2_6/ptodata/2/pubpna/us10J_PUBCOMB.seq:*
20: /cm2_6/ptodata/2/pubpna/us10H_PUBCOMB.seq:*
21: /cm2_6/ptodata/2/pubpna/us10I_PUBCOMB.seq:*
22: /cm2_6/ptodata/2/pubpna/us10N_PUBCOMB.seq:*
23: /cm2_6/ptodata/2/pubpna/us11A_PUBCOMB.seq:*
24: /cm2_6/ptodata/2/pubpna/us11_NEW_PUB.seq:*
25: /cm2_6/ptodata/2/pubpna/us60_NEW_PUB.seq:*
26: /cm2_6/ptodata/2/pubpna/us60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1308	100.0	1743	10 US-09-946-374-235	Sequence 235, App
2	1308	100.0	1743	14 US-10-006-856A-235	Sequence 235, App
3	1308	100.0	1743	14 US-10-184-644-451	Sequence 451, App
4	1308	100.0	1743	14 US-10-006-818A-235	Sequence 235, App
5	1308	100.0	1743	14 US-10-006-485A-235	Sequence 235, App
6	1308	100.0	1743	14 US-10-013-907A-235	Sequence 235, App
7	1308	100.0	1743	14 US-10-015-499A-235	Sequence 235, App

ALIGNMENTS

RESULT 1
US-09-946-374-235
Sequence 235, Application No. US20030073129A1
GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Boerstein, David
/ APPLICANT: Deanoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Guirney, Austin L.
/ APPLICANT: Hillian, Kenneth J.
/ APPLICANT: James
/ APPLICANT: Paconi, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watana, Cain K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.

/ TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
/ P18 REFERENCE: P2830P1CH
/ CURRENT APPLICATION NUMBER: US/09/946,374

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CM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 06:00:34 ; Search time: 114.5 Seconds

(without alignments)

8836.377 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 2444

Sequence: 1 atgcaaggacaggcaggag.....aaatccactaaatcctag 1308

Scoring table: BLOSSUM62

Xgapext 10.0 , Xgapext 0.5

Ygapext 10.0 , Ygapext 0.5

Fgapext 6.0 , Fgapext 7.0

Delext 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Command line parameters:

-MODEL:frame+ n2p.model -DEVL=rp

-Q=cgn2.1 -USPRO:spool_P/US0993180/runat_07102005_180815_18615/app_query.fasta_1.1479

-DB=A_Geneseq_16Dec04 -QMT=Esttan -SUPPXX=n2p.rag -MINMATCH=0.1 -LQPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=d:obtune2 -TRANS=human140.cdi

-LIST=45 -DOALIGN=00 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=sto -NORMEXT -HEAPSIZE=00 -MINLEN=0 -MAXLEN=2000000000

-USRP:US0993180@CCRN_1.1_154_Grunat_07102005_180815_18615 -NCPU=6 -TCPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_16Dec04:*

1: Geneseqp1880s:*

2: Geneseqp1590s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	Location/Qualifiers
1	2225	91.0	435	5	AAB25298		Aae25298 Human LSI	XX Key
2	2202	90.1	435	4	AA014912		AA014912 Human ser	FT Peptide
3	2124	86.9	417	4	AYY99407		AYY99407 Human PRO	FT Protein
4	2124	86.9	417	4	AAB66156		AAB66156 Protein	FT Binding-site
5	2124	86.9	417	4	AAU29249		AAU29249 Human PRO	FT Binding-site
6	2124	86.9	417	5	ABG70336		ABG70336 Human ser	FT Binding-site
7	2124	86.9	417	5	ABBB4928		ABBB4928 Human PRO	FT Binding-site
8	2124	86.9	417	5	ABB95334		ABB95334 Human ang	FT Binding-site
9	2124	86.9	417	6	ABU58625		ABU58625 Human PRO	FT Binding-site

ALIGNMENTS

RESULT 1

ID AAE25298 standard; protein; 435 AA.

XX

AC AAE25298;

XX

DT 30-OCT-2002 (first entry)

XX

DB Human LSI-01 protein.

KW Human; lymphocyte serine protease inhibitor; serpin-01; LSI-01; stroke; potassium channel beta subunit; cardiovascular; inflammatory disease; cancer; blood; immune; T-cell malignancy leukaemia; gastritis; metabolic; proliferative; emphysema; liver cirrhosis; arteriosclerosis; immunological disorder; rheumatoid arthritis; psoriasis; gene therapy; autoimmune infertility; vascular disease; microvascular disease; ulcer; diarrhoea; embolism; thrombosis; neurological; Alzheimer's disease; epilepsy; cyostatic; hepatotropic; thrombolytic; cerebroprotective; immunosuppressive; nootropic; neuroprotective; anticonvulsant; antinifertility.

XX

OS Homo sapiens.

Location/Qualifiers

1 .38 /label= Signal-peptide

39 .435 /note= "Human mature LSI-01 protein"

63 .80 /note= "Heparin binding region; This region is specifically referred in claim 34 of the specification"

125 .140 /note= "Heparin binding region; This region is specifically referred in claim 34 of the specification"

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nucleic - protein search, using frame_plus_n2p model

on: October 9, 2005, 14:18:29 ; Search time 34.5 Seconds
 (without alignments)
 7295.741 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Effect score: 2444

Sequence: 1 atgcaaggcaggccaggaggg.....aaaatccactaaatcttag 1308

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delet	7.0

Archived: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Maximum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

abase : PIR 79.*

1: **pir1:***
2: **pir2:***
3: **pir3:***
4: **pir4:***

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
					DB	Score
1	1047	42.8	415	2	A47224	thyroxine-binding
2	1044.5	42.7	418	2	A39567	thyroxine-binding
3	1023.5	42.1	412	2	A46421	thyroxine-binding
4	889.5	36.4	427	2	A49518	kalistatin precursor
5	852.5	34.9	406	2	A39339	protein C inhibitor
6	850	34.8	433	1	ITIHUC	alpha-1-antichymotrypsin-related
7	847	34.7	418	2	S23675	alpha-1-antichymotrypsin
8	833	34.1	418	2	JH0494	kalikrein-binding
9	829.5	33.9	417	2	S19724	serine proteinase
10	829.5	33.9	418	1	S131567	serine proteinase
11	821	33.6	408	2	S111320	alpha-1-antitrypsin
12	814.5	33.3	405	2	A39088	alpha-1-antitrypsin
13	806.5	33.0	413	2	A54988	alpha-1-antitrypsin
14	801	32.8	413	2	S54981	alpha-1-antitrypsin

115	800	32.7	413	2	JX0267
116	799	32.7	403	2	S08102
117	798	32.7	418	2	JX0129
118	795	32.5	411	1	ITRT
119	793	32.5	410	2	A45457
120	792	32.4	413	2	JX0154
221	790.5	32.3	412	2	S31505
222	788.5	32.3	406	2	JX0346
223	788	32.2	410	2	C39088
224	787	32.2	416	2	B29131
225	779	31.9	383	2	A36117
226	779	31.9	416	1	ITSH
227	778.5	31.9	405	2	A28321
228	777	31.8	430	2	A49120
229	774.5	31.7	413	2	149414
330	774.5	31.7	413	2	156481
331	771	31.5	409	1	ITBA
332	770.5	31.5	413	2	149470
333	769	31.5	416	2	S21057
334	768.5	31.4	413	2	149452
335	768	31.4	418	1	ITHU
336	767	31.4	413	2	860036
337	765.5	31.3	413	2	149472
338	759.5	31.1	413	2	149473
339	757	31.0	406	2	I53291
440	756.5	31.0	402	2	149471
441	744	30.4	388	2	B39088
442	705.5	28.9	410	1	I50494
443	697	28.5	412	1	ITMSC
444	692	28.3	369	2	149493
445	668	27.3	420	2	A28682

ALIGNMENTS

RESULT 1

A47224 thyroxine-binding globulin precursor - human
 C;Species: *Homo sapiens* (man)
 C;Accession: A47224 ; Sequence revision: 10-May-1996 #text_change 09-Jul-2004
 C;Accession: A47224 ; S39801 ; Ia6479 ; A13535 ; S22190
 R;Hayashi, Y.; Mori, Y.; Janssen, O.E.; Sunthornthepvarakul, T.; Weiss, R.E.;
 Mol. Endocrinol. 7, 1049-1060, 1993
 A;Title: Human thyroxine-binding globulin gene: complete sequence and transcript
 A;Reference number: A47224 ; MUID: 9409804 ; PMID: 8232304
 A;Accession: A47224 ; Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-15 <RES>
 A;Cross-references: UNIPROT: P05543 ; GB:L13470 ; NID: 9405513 ; PIDN: AAA16067.1 ; P
 R;Albari, M.T.; Kapdi, A.; Farmer, M.J.; Fitch, N.J.S.; McCann, K.P.; Kordestani,
 B.; Biophys. Acta 1216, 446-454, 1993
 A;Title: The structure of the human thyroxine binding globulin (TBG) gene

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 06:04:58 ; Search time 146.5 Seconds
9144.022 Million cell updates/sec
(without alignments)

Title: US-09-993-180-1_COPY_68_1375
Perfect score: 2444
Sequence: 1 atgcaaggacaggccaggag.....aaataccactaaatccatg 1308

Scoring table: BLOSSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Pgapop 6.0	Pgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MOPCL=frame_n2p model -DBWax1p
-Q=/FGN2.1/USPTO_spool/p/US0993180/runat_07102005_180816_18622/app_query.fasta_1.1479
-DB=Uniprot_03 -OPRT=fstan -SUPRTX=n2p_rup -MINMAXCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bins -STARTA=1 -ENDA=1 -MATRIX=b10sum62 -TRANS=0 -CDI=1 -LIST=15
-DOCA=1;GN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNN=15 -MODE=LOCAL
-USER=US0993180_OCGN_1.1 -L152@runat_07102205_180816_18622 -INCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DEL0P=6 -DELEXT=7

Database : UniProt 03:
1: uniprot_spref:
2: uniprot_trembl:
3: uniprot_trembl:
4: uniprot_trembl:
5: uniprot_trembl:
6: uniprot_trembl:
7: uniprot_trembl:
8: uniprot_trembl:
9: uniprot_trembl:
10: uniprot_trembl:
11: uniprot_trembl:
12: uniprot_trembl:
13: uniprot_trembl:
14: uniprot_trembl:
15: uniprot_trembl:
16: uniprot_trembl:

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P29622 homo sapien
Q86tr9 homo sapien
P01011 homo sapien
Q9mg66 sus scrofa
Q9un99 homo sapien
P05154 homo sapien
Q03734 mus musculus
P70458 mus musculus
Q8cie0 mus musculus
Q8bu50 mus musculus
Q9y1b8 xenopus lae
Q8bvn1 mus musculus
Q9n212 bos taurus
Q78y20 xenopus lae
Q91wp6 mus musculus
Q62258 mus musculus
Q60552 mesocricetus
Q54758 tamias sibiricus
Q7tp55 rattus norvegicus
P29621 mus musculus
Q60395 apodemus sylvaticus
P09006 rattus norvegicus
Q88292 rattus norvegicus
Q66h15 rattus norvegicus
Q54763 callosciurus
Q76hn9 tamias sibiricus
Q54760 tamias sibiricus
P22225 cavia porcellus
Q62663 oryzotomys

Result 1

Q86wd7	PRELIMINARY;	PRT;	435 PA.
1D Q86wd7;			
AC 01-JUN-2003	(TREMBLrel: 24, Created)		
DT 01-JUN-2003	(TREMBLrel: 24, Last sequence update)		
DT 01-MAR-2004	(TREMBLrel: 26, Last annotation update)		
DE Germinal center B-cell expressed transcript 1 isoform A.			
GN Name=GCBT1;			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1];			
RP SEQUENCE FROM N.A.			
RX MEDLINE=22702315; PubMed=12819018;			
RA Pan Z., Shen Y., Du C., Zhou G., Rosenwald A., Staudt L.M., Greiner T.C., McKeithan T.W., Chan W.C.,			
RT "Two newly characterized germlinal center B-cell-associated genes, GCBT1 and GCBT2, have differential expression in normal and neoplastic B cells.";			
RT Am. J. Pathol. 163:135-144 (2003).			
RL CC 1- SIMILARITY: Belongs to the serpin family.			
DR EMBL; Y220118; AAO62421; -.			
EN DR HSP; P05154; 1LQ8.			
RN DR GO; GO:0004867; P:serine-type endopeptidase inhibitor activity; IEA.			
RA DR Interpro; IPR000295; Prot inh Serpin.			
RA DR Interpro; IPR000215; Prot_inh_serpin.			
RA DR PF00079; Serpin; 1.			
RA DR PRINTS; PRO0780; LEUSERPNNI.			
RA DR SMART; SM00093; SERPIN; 1.			
RA DR PROSITE; PS00284; SERPIN; UNKNOWN_1.			
RA KW Protease inhibitor; Serine protease inhibitor; Serpin.			
RA SQ SEQUENCE 435 AA; 48569 MW;			

Alignment Scores:
Pred. No.: 6.44e-153
Score: 218.600
Percent Similarity: 98.85%
Best Local Similarity: 98.62%

ALIGNMENTS

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P29622 homo sapien
Q86tr9 homo sapien
P01011 homo sapien
Q9mg66 sus scrofa
Q9un99 homo sapien
P05154 homo sapien
Q03734 mus musculus
P70458 mus musculus
Q8cie0 mus musculus
Q8bu50 mus musculus
Q9y1b8 xenopus lae
Q8bvn1 mus musculus
Q9n212 bos taurus
Q78y20 xenopus lae
Q91wp6 mus musculus
Q62258 mus musculus
Q60552 mesocricetus
Q54758 tamias sibiricus
Q7tp55 rattus norvegicus
P29621 mus musculus
Q60395 apodemus sylvaticus
P09006 rattus norvegicus
Q88292 rattus norvegicus
Q66h15 rattus norvegicus
Q54763 callosciurus
Q76hn9 tamias sibiricus
Q54760 tamias sibiricus
P22225 cavia porcellus
Q62663 oryzotomys

Result No. Score Query % Description

1	2186	89.4	435	2 Q86wd7 homo sapien
2	2124	86.9	417	2 Q6wd9 homo sapien
3	1867	76.4	370	2 Q86vp9 homo sapien
4	1690	69.1	337	2 Q86yp7 homo sapien
5	1640	67.1	335	2 Q86wd5 homo sapien
6	1473	60.3	334	2 Q86vp6 homo sapien
7	1429	58.5	286	2 Q86wd4 homo sapien
8	1347	55.1	418	2 Q9d7d2 mus musculus
9	1075	43.3	412	1 THBG_PIG
10	1047	42.8	415	1 THBG_HUMAN
11	1045	42.7	418	1 THBG_RAT
12	1042	42.6	415	1 THBG_PANTHERA
13	1040	42.6	411	1 THBG_BOVINUS
14	1029.5	42.1	412	1 THBG_SHEEP
15	1021.5	41.8	418	1 THBG_MOUSE
16	896.5	36.7	440	2 Q86ui7 homo sapien

SUMMARIES

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P29622 homo sapien
Q86tr9 homo sapien
P01011 homo sapien
Q9mg66 sus scrofa
Q9un99 homo sapien
P05154 homo sapien
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P70458 mus musculus
Q8cie0 mus musculus
Q8bu50 mus musculus
Q9y1b8 xenopus lae
Q8bvn1 mus musculus
Q9n212 bos taurus
Q78y20 xenopus lae
Q91wp6 mus musculus
Q62258 mus musculus
Q60552 mesocricetus
Q54758 tamias sibiricus
Q7tp55 rattus norvegicus
P29621 mus musculus
Q60395 apodemus sylvaticus
P09006 rattus norvegicus
Q88292 rattus norvegicus
Q66h15 rattus norvegicus
Q54763 callosciurus
Q76hn9 tamias sibiricus
Q54760 tamias sibiricus
P22225 cavia porcellus
Q62663 oryzotomys

Result No. Score Query % Description

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11	1045	42.7	418	1 THBG_RAT
12	1042	42.6	415	1 THBG_PANTHERA
13	1040	42.6	411	1 THBG_BOVINUS
14	1029.5	42.1	412	1 THBG_SHEEP
15	1021.5	41.8	418	1 THBG_MOUSE
16	896.5	36.7	440	2 Q86ui7 homo sapien

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P29622 homo sapien
Q86tr9 homo sapien
P01011 homo sapien
Q9mg66 sus scrofa
Q9un99 homo sapien
P05154 homo sapien
Q03734 mus musculus
P70458 mus musculus
Q8cie0 mus musculus
Q8bu50 mus musculus
Q9y1b8 xenopus lae
Q8bvn1 mus musculus
Q9n212 bos taurus
Q78y20 xenopus lae
Q91wp6 mus musculus
Q62258 mus musculus
Q60552 mesocricetus
Q54758 tamias sibiricus
Q7tp55 rattus norvegicus
P29621 mus musculus
Q60395 apodemus sylvaticus
P09006 rattus norvegicus
Q88292 rattus norvegicus
Q66h15 rattus norvegicus
Q54763 callosciurus
Q76hn9 tamias sibiricus
Q54760 tamias sibiricus
P22225 cavia porcellus
Q62663 oryzotomys

Result No. Score Query % Description

1	2186	89.4	435	2 Q86wd7 homo sapien
2	2124	86.9	417	2 Q6wd9 homo sapien
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12	1042	42.6	415	1 THBG_PANTHERA
13	1040	42.6	411	1 THBG_BOVINUS
14	1029.5	42.1	412	1 THBG_SHEEP
15	1021.5	41.8	418	1 THBG_MOUSE
16	896.5	36.7	440	2 Q86ui7 homo sapien

13 768 31.4 418 1 US-08-477-108A-3
 14 768 31.4 418 2 US-10-477-112-3
 15 768 31.4 418 4 US-10-030-330-3
 16 768 31.4 418 5 PCT/US93/08322-3
 17 763 31.2 418 4 US-10-000-489-92
 18 757 31.0 394 1 US-08-002-202-11
 19 757 31.0 394 2 US-08-553-488A-1
 20 756 30.9 394 1 US-08-002-202-9
 21 756 30.9 394 3 US-08-481-534-11
 22 755 30.9 394 3 US-08-481-534-9
 23 755 30.9 394 1 US-08-002-202-13
 24 755 30.9 414 3 US-08-481-534-13
 25 754.5 30.9 363 4 US-09-755-665-58
 26 754 30.9 363 4 US-08-002-202-19
 27 754 30.9 414 3 US-08-481-534-11
 28 751 30.7 394 1 US-08-002-202-5
 29 751 30.7 394 3 US-08-023-333-1
 30 750 30.7 394 3 US-08-481-534-6
 31 749 30.6 414 1 US-08-002-202-17
 32 749 30.6 414 3 US-08-481-534-17
 33 694.5 28.4 421 4 US-09-949-016-8165
 34 690.5 28.3 414 4 US-09-755-665-14
 35 690.5 28.3 414 4 US-09-755-665-55
 36 690.5 28.3 414 4 US-09-755-665-56
 37 690.5 28.3 415 4 US-09-461-345-134
 38 690.5 28.3 415 4 US-10-012-542-134
 39 690.5 28.3 415 4 US-10-115-123-134
 40 668 27.3 420 4 US-09-949-016-6705
 41 651 26.6 351 4 US-10-000-489-50
 42 645.5 26.4 361 4 US-09-755-665-57
 43 562 23.0 366 4 US-09-716-793A-2
 44 552 22.6 499 4 US-09-054-272-36
 45 552 22.6 499 4 US-09-054-272-51
 45 552 22.6 499 4 US-09-054-272-51

RESULT 1
 US-09-912-628-5
 ; Sequence 5, Application US/09912628
 ; Patent No. 6753164
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
 ; CURRENT APPLICATION NUMBER: US/09/912,628
 ; FILE REFERENCE: PTO01P2
 ; CURRENT FILING DATE: 2001-07-26
 ; PRIORITY APPLICATION NUMBER: PCT/US01/02484
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIORITY APPLICATION NUMBER: 60/178,769
 ; PRIORITY APPLICATION NUMBER: PCT/US00/05082
 ; PRIORITY FILING DATE: 2000-02-29
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-912-628-5

ALIGNMENTS

Alignment Scores: Length: 435
 Pred. No.: 4,41e-203 Matches: 431
 Score: 2202.00 Conservative: 0
 Percent Similarity: 99.08% Mismatches: 4
 Best Local Similarity: 99.08% Indels: 0
 Query Match: 90.10% Gaps: 0
 DB: 4 DB:

US-09-993-180-1_COPY_68_1375 (1-1308) x US-09-912-628-5 (1-435)
 1 ATGCAAGGACAGGGCAGGAGAAAGGGAACTCTGCAAGACATATTGTTCCAAAATGGCA 60

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GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 9, 2005, 15:16:48 ; Search time 121 Seconds

(without alignment) Seconds
8994.176 Million cell updates/sec

Title: US-09-993-180-1_COPY_68_1375

Perfect score: 2444

Sequence: 1 atgcaggacaggcaggag.....aaatccactaaatccctag 1308

Scoring table: BLOSUM62

Xgap0 10.0 , Xgapext 0.5

Ygap0 10.0 , Ygapext 0.5

Fgap0 6.0 , Fgapext 7.0

Del0 6.0 , Delext 7.0

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 3708224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Command line parameters:

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Database : Published_Applications_AA.*

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3: /cgn2_6/ptodata/2/pubpa/US06_PUB.pep.*

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6: /cgn2_6/ptodata/2/pubpa/PCRTS_PUBCOMB.pep.*

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17: /cgn2_6/ptodata/2/pubpa/US10B_PUBCOMB.pep.*

18: /cgn2_6/ptodata/2/pubpa/US10B_NEW_PUB.pep.*

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20: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB.pep.*

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22: /cgn2_6/ptodata/2/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2225	91.0	435	10	US-09-993-180-2		Sequence 2, Appl1
2	2202	90.1	435	9	US-09-912-628-5		Sequence 5, Appl1
3	2124	86.9	417	13	US-09-946-374-236		Sequence 236, App
4	2124	86.9	417	13	US-10-092-586-452		Sequence 452, App
5	2124	86.9	417	14	US-10-174-590-452		Sequence 452, App
6	2124	86.9	417	14	US-10-176-758-452		Sequence 452, App
7	2124	86.9	417	14	US-10-175-737-452		Sequence 452, App
8	2124	86.9	417	14	US-10-174-581-452		Sequence 452, App
9	2124	86.9	417	14	US-10-176-483-452		Sequence 452, App
10	2124	86.9	417	14	US-10-176-749-452		Sequence 452, App
11	2124	86.9	417	14	US-10-176-914-452		Sequence 452, App
12	2124	86.9	417	14	US-10-176-915-452		Sequence 452, App
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14	2124	86.9	417	14	US-10-180-557-452		Sequence 452, App
15	2124	86.9	417	14	US-10-173-700-452		Sequence 452, App
16	2124	86.9	417	14	US-10-174-572-452		Sequence 452, App
17	2124	86.9	417	14	US-10-176-573-452		Sequence 452, App
18	2124	86.9	417	14	US-10-176-913-452		Sequence 452, App
19	2124	86.9	417	14	US-10-180-552-452		Sequence 452, App
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32	2124	86.9	417	14	US-10-176-750-452		Sequence 452, App
33	2124	86.9	417	14	US-10-176-985-452		Sequence 452, App
34	2124	86.9	417	14	US-10-176-987-452		Sequence 452, App
35	2124	86.9	417	14	US-10-176-992-452		Sequence 452, App
36	2124	86.9	417	14	US-10-176-993-452		Sequence 452, App
37	2124	86.9	417	14	US-10-184-650-452		Sequence 452, App
38	2124	86.9	417	14	US-10-176-991-452		Sequence 452, App
39	2124	86.9	417	14	US-10-176-995-452		Sequence 452, App
40	2124	86.9	417	14	US-10-173-697-452		Sequence 452, App
41	2124	86.9	417	14	US-10-173-705-452		Sequence 452, App
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44	2124	86.9	417	14	US-10-174-586-452		Sequence 452, App
45	2124	86.9	417	14	US-10-175-747-452		Sequence 452, App

ALIGNMENTS

RESULT 1
US-09-993-180-2

1 Sequence 2, Application US/0993180
; Publication No. US2003054445A1

; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPH CELLS, LSI-01
; FILE REFERENCE: D0051.NP
; CURRENT APPLICATION NUMBER: US/09/993_180
; PRIOR APPLICATION NUMBER: 2001-11-14
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,434
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 46
; PRIOR APPLICATION NUMBER: US 60/257,610
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/282,745
; PRIOR FILING DATE: 2001-04-10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2